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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpna/f

2: /cgn2_6/ptodata/1/pubpna/f

3: /cgn2_6/ptodata/1/pubpna/f

4: /cgn2_6/ptodata/1/pubpna/f

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18: /cgn2_6/ptodata/1/pubpna/f

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10: /cgn2_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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                                                        9 US-10-267-311-50

10 US-09-700-927A-42

10 US-09-700-988-1

10 US-09-960-428-13

10 US-09-841-13-28-13

10 US-09-841-13-28-26-65

9 US-09-731-626-65

9 US-10-267-311-28

9 US-10-267-311-33-23

9 US-10-267-311-16

9 US-09-738-626-131-16

9 US-09-738-626-131-16

9 US-09-738-626-131-16

9 US-09-738-626-131-16

9 US-09-738-626-2986

9 US-10-068-059-7

US-10-068-059-7

US-10-068-059-11
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Sequence 1, Appl
Sequence 1, Appl
Sequence 13, Appl
Sequence 380, Appl
Sequence 266, App
Sequence 20, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 9, Appl
Sequence 11, Appl
Sequence 5, Appl
Sequence 5, Appl
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Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 11, Appl
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GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER: OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50
SEQ ID NO 50
SEQ ID NO 50
SEQ ID NO 50
FENTURE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
FEATURE:
MAME/KEY: CDS
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; LOCATION: (1)...(1923)
US-10-267-311-50
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Best Local Similarity 77.5%;
Matches 1258; Conservative
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                                                            61 ATCCTTGCAGATACTGTTAAAGTAACTTTGGGACCAAAAGGTCGCAATGTCGTTCTTGAA 120
                                                                                                                                                                                                                   15 ATGGCAAAAGAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGGGAGTTGAT 74
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                                                                                                                                                                                1 ATGGCAAAAGAAATTAAATTTTCATCAGATGCCCGTTCAGCTATGGTCCGTGGTGTCGAT 60
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10 US-09-938-842A-216
10 US-09-938-892A-1623
11 US-09-938-892A-1623
12 US-09-938-892A-161
13 US-09-938-626-667
14 US-09-938-626-667
15 US-09-938-626-667
16 US-09-938-626-667
17 US-09-938-626-637
18 US-09-938-626-637
19 US-09-880-505-116
10 US-09-934-300-6303
17 US-09-934-300-6303
18 US-09-880-505-115
19 US-09-938-508-715
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US-09-88
US-10-05
US-10-05
US-09-88
US-09-93
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Pred. No. 2.2e-244;
0; Mismatches 366;
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1926 640685 1635 1635 1017 1017 11017 12847 1623 1623

Query Match

Length

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Title: Perfect score:

US-09-001-737-7 1661

Run on OM nucleic -

nucleic search, using sw model

Scoring table: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

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1095 GAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGA 1154
                                                                      1141 GCCGCAACTGAAACTGAGTTGAAAGAAATGAAACTCCGCATTGAAGATGCCCTCAACGCT
                                                                                                                                                               1081 GAAAAATTGCAAGAACGCTTGGCCAAATTGTCAGGTGGTGTAGCGGTTATTAAGGTCGGA
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                                                                                                                  GCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCT
  ACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTT
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TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 42:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                          APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-MAY-2000
CLASSIFICATION: <UKNOWND-
PRIOR APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY_AGENT INFORMATION:
NAME: Kenley K. HOOVET
                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb.

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                            NAMÉ: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides
NUMBER OF SEQUENCES: 982
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Best Local :
                                                                                                                       1144
                                                                                                                                                                                                                                                         1024
                                                 1204 GACCGCCGCAAAGCGATGCTTGAAGATATTGCTATTTTAACAGGTGGTACAGTAATCACT 1263
                                                                                                                                                                                1084 CAAAGCCGTCCACTATTGATTATTGCGGATGATGTTGATGGGGGAAGCTCTACCAACATTA 114:
915 GAGGATCTAGGACTTGAAATAAAGATGCCTACAATGACAGCCCTTGGACAGGCTGCTAAG 974
                                                                                      855
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                                                                                  GATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACA 914
                                                                                                                   GTATTGAACAAAATCCGTGGTACATTTAATGTTGTCGCAGTAAAAGCGCCCAGGATTTGGT 1203
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91; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                           TTACAAAATGCAGCTTCTGTGTCAGCTTTATTAATAACAACTGAAGCAGTTGTTGCAGAC 1923
                                                                                                                   CTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAAT 1574
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US-09-790-988-1
US-09-790-988-1
Sequence 1, Application US/09790988
Patent no. US20020127687A1
GENERAL INFORMATION
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: UP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET: 2.1
LENGTH: 640681
TYPE: DNA
CORGANISM: BUChnera sp.
US-09-790-988-1
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                                                 GCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGT 1094
                                                                                                  GTTGTTATTAGCAAAGACACTACAACTATTATTGGTGGTGTAGGAGAAAAACACTCCATT
                                                                                                                                                                                                                                                                                                    GATCGTCGTAAAGCAATGTTACAAGATATTTCAATTCTTACTGGTGGTTCTGTTATCTCT 19620
                                                                                                                                  ATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATT 1034
                                                                                                                                                                                                 GAAGAATTAGCTATGGAAATTAGAAAATCTACTTTAGAAGATTTAGGACAAGCAAAACGT 19680
                                                                                                                                                                                                                                                                                                                                                                                                      GTAGTTAATTCAATGAGGAGTATTGTAAAAGTCGCAGCAGTAAAAGCACCTGGATTTGGT 19560
                                                                                                                                                                                                                                             GAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAG
                                                                                                                                                                                                                                                                                                                                       GATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACA 914
                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCGAGGATTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTATTGCTCAGGTCGCTGCAGTATCATCACGCTC---TGAAAAAGTTGGAGAGTATATC 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGATAAAAAATATCTAATGTTCGTGAAATGTTACCAATATTAGAATCTGTTGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAA 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGAAGCAATGGAAAAAGTTGGTAATGACGGAGTTATTACAGTAGAAGAAGGTACAGGT 19260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGTTACCATCGAAGAATCTCGAGGT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAATTACACAAGTTGGTACTATTTCTGCAAATGCAGATGAAAAAGTTGGTTCTTTAATT 19200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGTTATCAGTGCTGTAGAAGAATTAAAACATTTATCTGTACCATGTTCTGATTCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTTTAAAAGCAGTAGCAGCTGGTATGAATCCAATGGATCTGAAACGTGGAATTGATAAA 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGCAGCAGGTGATGGTACCACAACAGCAACATTATTAGCACAATCTATAGTAAATGAA 19020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTTGACACAAGCCATTGTTCATGAA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATAAATTCGAAAACATGGGAGCTCAAATGGTAAAAGAAGTTGCATCAAAAGCAAAC 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAAT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTTTGGAGCACCTAGTATTACTAAAGATGGTGTATCCGTAGCCCGTGAAATTGAATTA 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAATTA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAGCAGATGCAGTAAAAGTGACTTTAGGACCAAAAGGTAGAAATGTAGTTCTAGATAAA 18840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGCCGCAATGTTGTTCTTGAAAAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTAAAGATGTAAAATTTGGAAATGAAGCCCGCATTAAAATGCTTCGTGGAGTTAATGTA 18780
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 986; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Roche Diagnostics GmbH
TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in prokary
FILE REFERENCE: 5272/00/
CURRENT APPLICATION NUMBER: US/09/960,428
CURRENT FILLING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
TENOTH: 2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09960428 Patent No. US20020115147A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20281 GACTTGCCTAAAGAAGATA 20299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20221 GCTTTACAGTATGCTGCTTCTGTCGCTGGTCTAATGATCACAACAGAATGTATGGTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20161 GATGAATATGGTGACATGATAGATTTTGGTATATTAGATCCAACTAAAGTTACACGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20101 TCTGTAGTTACAAACAATGTAAAAGACGGAAAAGGTAACTATGGTTACAATGCAGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19981 GCAGGGAAAATAGCTGATTTACGTGGTCAAAATGAAGATCAGAACGTAGGTATTCGAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1572 AATAAACCTGAACCAGCTA 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1512 GCGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1452 GGTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCA 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1392 TCCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACA 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1095 GAAAAACTACAAGAACGITTGGCGAAATTAGCTGGTGGTGGTGTGAGCTGTTATCAAAGTAGGA 1154
198 GAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAAT
                                                                                                                                                                                                                                 478
                                                               598 TCTTTCGGTGCACCGACCATCACCAAAGATGGTGTTTCCGTTGCTCGTGAAATCGAACTG
                                                                                                                                                                                                                                                      18 GCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGGAGTTGATATG
                                                                                             GCTTTTGGTTCTCCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATTCGAATTA 197
                                                                                                                                            CTGGCAGATGCAGTGAAAGTTACCCTCGGTCCAAAAGGCCGTAACGTAGTTCTGGATAAA
                                                                                                                                                                      TTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAAGGGCGCAATGTTGTTCTTGAAAAA 137
                                                                                                                                                                                                                          GCTAAAGACGTAAAATTCGGTAACGACGCTCGTGTGAAAATGCTGCGCGGCGTAAACGTA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCGTGCAGCTGTAGAAGAAGGTGTAGTTGCTGGAGGTGGTGTTGCATTAGTGCGTGTA 1998(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTT 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGCTACAGAAGTAGAAATGAAAAGAAAAAAAGCTCGTGTTGAAGATGCATTACATGCT 19920
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                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                       35.5%; Score 589.8; DB 10; 61.3%; Pred. No. 1.7e-134; tive 0; Mismatches 617;
                                                                                                                                                                                                                                                                                                                                                 Length 2155;
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1078 TACTTCATCAACAAGCCGGAAACTGGCGCAGTAGAACTGGAAAGCCCGTTCATCCTGCTG 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    675 ACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTTGAGGAAGTTCTTAAA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 615 TACATGGTCACAGACAATGAAAAATGGTTGCAGACCTTGAAAACCCCATTTATCTTAATC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555 ATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAA 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 TCAGAAGCTATGGACCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 GGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          958 GCTGAAGCGATGGACAAAGTCGGTAAAGAAGGCGTTATCACCGTTGAAGACGGTACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 GCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               778 GGTCTGAAAGCTGTTGCTGCGGGCATGAACCCGATGGACCTGAAACGTGGTATCGACAAA
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                                                                                                                                                                                                  GAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGA 1154
                                                                                                                                                                                                                                                                                                                                                                                            CAGGGCCGTGTTGCTCAGATCCGTCAGCAGATTGAAGAAGCAACTTCTGACTACGACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACA 914
             GCGTCTAAACTGGCTGACCTGCGTGGTCAGAACGAAGACCAGAACGTGGGTATCAAAGTT
                                                      ATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACA---TT 1331
                                                                                                                                      ACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGTAGCACACTTATTACGGTT 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGT 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCGTCGTAAAGCTATGCTGCAGGATATCGCAACCCTGACTGGCGGTACCGTGATCTCT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTGTTAACACCATGCGTGGCATCGTGAAAGTCGCTGCGGTTAAAGCACCGGGCTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGT 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGCAAACCGCTGCTGATCATCGCTGAAGATGTAGAAGGCGAAGCGCTGGCAACTCTG 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTT 794
                                                                                                                                                                                                                                                                                               GAAAAACTGCAGGAACGCGTAGCGAAACTGGCAGGCGGCGTTGCAGTTATCAAAGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGTGATCAACAAAGACACCACCACTATCATCGATGGCGTGGAGGAAGCTGCAATC 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATT 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGAGATCGGTATGGAGCTGGAAAAAGCAACCCTGGAAGACCTGGGTCAGGCTAAACGT 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGACAAGAAATCTCCAACATCCGCGAAATGCTGCCGGTTCTGGAAGCTGTTGCCAAA 1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTATTGCTCAGGTCGCTGCAGTATCATCACGCTC---TGAAAAAGTTGGAGAGTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGTTACCGCTGCAGTTGAAGAACTGAAAGCGCTGTCCGTACCATGCTCTGACTCTAAA
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; ORGANISM: Chlamydia pneumoniae
US-09-841-132-380
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US-09-841-132-380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 59.5
Matches 957; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bhatla, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: U5/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 TTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCCCAATGTTGTTCTTGAAAAA 137
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                                                                                                          GGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACA 377
                                                                                                                                                                                                                                                                                            GAAGATCATTTTGAAAACATGGGAGCAAAATTTGGTGTCTGAAGTGGCTTCTAAAACCAAT 257
                                                                       GGTCTAAGAAATGTCACTGCCGGTGCCAATCCTATGGACCTAAAAAGAGGTATCGACAAA 366
                                                                                                                                                                                                                                                                 GAAGACAAACATGAAAACATGGGCGCTCAGATGGTAAAAGAAGTCGCCAGCAAAACTGCT
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20020061848A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %; Score 530.4; DB 10;
%; Pred. No. 5.2e-120;
0; Mismatches 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 15;
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1326 AACATTGTGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTAC 1385
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                                                                                                                                                                                                                                                                    1327 CGTATTATTCTAAAAAGCATTAACAGCTCCATTAAAGCAAATTGCAAGTAACGCAGGTAAA 1386
                                                                                                                                                                                                                                                                                                                                                                                                          1267 ATCCCTACACTAGAAGCTTTCCTTCCTATGCTAGCAAACGAAGACGAAGCTATTGGTACT
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1447 TTACGTGACGCTTATACAGATATGATTGACGCAGGAATTTTAGATCCAACTAAAGTGACT 1506
                                           1446 GCAACAGGTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACA 1505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: P824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8504
INFORMATION FOR SEO ID NO: 266;
SEQUENCE CHARACTERISTICS:
LENGTH: 1017 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.1%; Score 483.6; DB 7; Length 1017; Best Local Similarity 67.2%; Pred. No. 1.2e-108; Matches 681; Conservative 2; Mismatches 331; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 266, Application US/08781986A Publication No. US20030054436A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
2IF: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette; 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTMARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1566 GTTGCTAATAAACCTGAA----CCAGCTACGCCAGCGCCAGCGAATGCCA 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1506 CGATCAGCGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTT 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1567 ATCGCTGATATCCCAGAAGAAGAAATCTTCTTCAGCTCCAGCGATGCCA 1614
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548 TCGAGGTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCT
                                        428 TGGCAAGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGA 487
                                                                                                                                                                                                                                                                                                                                     308 TGTTCATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Marvin:
                                                                                                                              121 AAATAAAAATGAAATTGCGCAAGTAGGTGCGATTTCAGCAGCAGATGAAGAAATTGGACG 180
                                                                                                                                                                                                                                                            368 CATTGAAACAGCAACAGCAACAGCTGTTGAAGCCCTTGAAAGCCATTGCTCAACCTGTATC 427
                                                                                                                                                                                                                      61 TATCGACAAAGCAGTTAAAGTTGCTGTTGAAGCGTTACATGAAAATTCTCAAAAAGTTGA 120
                                                                                                                                                                                                                                                                                                    1 TTTCCAAGAAGGCTTGAAAAATGTTWCAAGTGGTGCGAMCCCAGTTGGTTTACGACAAGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/781,986A
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Indels Length 1614;

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APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, MANOKO
APPLICANT: IKEDA, KIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                Sequence 665, Application US/09738626
Sequence 665, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACGGTTATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGGGGATGATGCTACTGG 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMATGTTTACCAMAAAGTAAGTGAAATTGAAGCTGAAGGTGACATTGAAACAGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATGCTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTAT 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTAGGAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCT 1207
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PRIOR FILING DAYE: 2000-04-07
PRIOR PPLICATION NUMBER: JP 00/280988
PRIOR FILING DAYE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 665
LENGTH: 1614
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-665
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Best Local Similarity 56.4%;
Matches 890; Conservative
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GATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACA
                                              GTTGTGAACTCCATCCGCAAGACCATCAAGGTCGTTGCAGTGAAGTCCCCTTACTTCGGT
                                                                                                                                   TCCAACCGTCCTTTGCTGATCATCGCAGAGACGTCGAGGGCGAGCCTTTGCAGACCCTG
                                                                        GTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGT 854
                                                                                                                                                                                                                             GTTCGCAACAAGATTTCTTCCCTCCCAGACTTCCTCCCATTGCTGGAGAAGGTTGTGGAG
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                                                                                                                                                                              ACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTT 794
                                                                                                                                                                                                                                                                                                                  TATTTCATCAACGACAACGACACTCAGCAGGCTGTCCTGGACAACCCTGCAGTGCTGCTT
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Pred. No. 8.4e-104;
0; Mismatches 683;
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CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-70
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
UMMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 2847
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US:10-267-311-20
                                                                                                                                                                                                                                           Sequence 20, Application US/10267311

Publication No. US20030050469A1

GENERAL INFORMATION:

APPLICANT: Slegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGTGCTTCGTGCTCTAGAAGAGCCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAA 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTT 1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAAGGCAGAAGAGCGTTTGGCTAAGCTCTCCGGTGGTATTGCTGTCATCCGCGTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACATCTGGACTTTGACCGT 1094
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; LOCATION: (1)...(2844)
US-10-267-311-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.8%;
Best Local Similarity 55.9%;
Matches 878; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                        912 ACAGAGGATCTAGGACTTGAATTAÄAAGATGCTACAATGACAGCCCTTGGACAGGCTGCT
                                                                                                                                                                                                                                                                                                                                      672 ATCACGGATAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTT
                                                                                                                                                                                                                                                             732 AAAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACC
                                                                                                                                                                                                                                                                                                                                                                                          658 GGGTACTTCGTGACCGACCCGGAGCGTCAGGAGGCGGTCCTGGAGGACCCCCTACATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                     612 CAATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTA 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 GGTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 ATCTCAGAAGCTATGGAGCGTGTGGGGAACGATGGTGTGATTACCATCGAAGAATCTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 AAGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTTGGAGAGTAT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 CGCGAGGGCCTGCGCAACGTCGCGGCCGGCCCAACCCGCTCGGTCTCAAACGCGGCATC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 CATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 ACCGATGACGTCGCCGGTGACGGCACCACGGCCACCGTGCTGGCCCAGGCGTTGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598 ACCTTTGGGCTGCAGCTCGAGCTCACCGAGGGTATGCGGTTCGACAAGGGCTACATCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 AAGGAGCAGATTGCGGCCACCGCAGCGATTTCGGCGGGTGACCAGTCCATCGGTGACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 GAGCTGGAGGATCCGTACGAGAAGATCGGCGCCGAGCTGGTCAAAGAGGTAGCCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 GAATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 GAAAAGAAGTGGGGTGCCCCCACGATCACCAACGATGGTGTGTCCATCGCCAAGGAGATC
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                                                                                                                                  CTGGTCGTCAACAAGATCCGCGGCACCTTCAAGTCGGTGGCGGTCAAGGCTCCCGGCTTC
                                                                                                                                                                          CTTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGGCCAGGATTT 851
                                                                                                                                                                                                                     GGAGCCGGTAAGCCGCTGCTGATCATCGCCGAGGACGTCGAGGGCGAGGCGCTGTCCACC
                                                                                                                                                                                                                                                                                                        CTGGTCAGCTCCAAGGTGTCCACTGTCAAGGATCTGCTGCCGCTGCTCGAGAAGGTCATC
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Pred. No. 4.9e-103;
0; Mismatches 694;
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Length 1947;

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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
INUMBER: TILING DATE: 1999-07-08
INUMBER: FASTED FOR WINDOWS Version 4.0
SOFTMARE: FASTED FOR WINDOWS Version 4.0
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Sequence 28, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
                                                                                            TYPE: DNA
                                                        ORGANISM: Artificial Sequence FEATURE:
                                OTHER INFORMATION: fusion sequence
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US-10-267-311-28
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Best Local Similarity 55.8%;
Matches 877; Conservative
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                                                                     ACAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCT
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Pred. No. 9.9e-103;
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APPLICANT: EISENDERG, DAVID
APPLICANT: MISCOTTE, SERGIO H.
APPLICANT: MISCOTTE, SERGIO H.
APPLICANT: MISCOTTE, SERGIO H.
APPLICANT: MISCOTTE, SERGIO H.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND TITLE OF INVENTION: INVERACTIONS OF PROTEINS BY FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT APPLICATION NUMBER: PCT/US00/02246
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR APPLICATION NUMBER: 60/119,531
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 1999-01-03
PRIOR PRIOR APPLICATION NUMBER: 60/116,206,
PRIOR APPLICATION NUMBER: 60/116,593
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-03-14
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/114,092
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PRIOR APPLICATION NUMBER: 60/114,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/114,092
PRIOR FILING DATE: 1999-05-14
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PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
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US-09-712-363-23
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Patent No. US20020164588A1
GENERAL INFORMATION:
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ORGANISM: Mycobacterium tuberculosis US-09-712-363-23
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PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 23
LENGTH: 1623
TYPE: DNA
TYPE: DNA
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Best Local Similarity 55.8%;
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                                                                                                                                                                            ACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTT
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                                                          GTCGTCAACAAGATCCGCGGCACCTTCAAGTCGGTGGCGGTCAAGGCTCCCGGCTTCGGC
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Pred. No. 2e-102;
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Sequence 3, Application US/10267311

Sequence 3, Application US/10267311

Sequence 3, Application US/20030050469A1

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Siegel, Marvin

APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO

FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/99/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US/09/613,757

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR APPLICATION NUMBER: US 60/143,757
                                                       NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1623
TYPE: DNA
                ORGANISM: Artificial Sequence FEATURE:
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US-10-267-311-3
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Best Local Similarity 55.8%;
Matches 875; Conservative
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GAAGAGGTCGGCCTGACGCTGGAGAACGCCGACCTGTCGCTAGGCAAGGCCCGCAAG
                                                                            GACCGCCGCAAGGCGATGCTGCAGGATATGGCCATTCTCACCGGTGGTCAGGTGATCAGC 900
                                                                                                                                                         GTCGTCAACAAGATCCGCGGCACCTTCAAGTCGGTGGCGGTCAAGGCTCCCGGCTTCGGC 840
                                                                                                                                                                                        GTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCCAGGATTTTGGT 854
                                                                                                                                                                                                                                         GCCGGTAAGCCGCTGCTGATCATCGCCGAGGACGTCGAGGGCGAGGCGCTGTCCACCCTG 780
                                                                                                                                                                                                                                                                                                                        GTCAGCTCCAAGGTGTCCACTGTCAAGGATCTGCTGCCGCTGCTCGAGAAGGTCATCGGA 720
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RESULT 12

US-10-267-311-16

Sequence 16, Application US/10267311

Publication No. US20030050469A1

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall

APPLICANT: HIZZEN, Lee A.

TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO

FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR APPLICATION NUMBER: US/09/613,757

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 12000-07-10

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 12000-07-10

SOFTWARE: FASTSED for Windows Version 4.0

SEQ ID NO 16
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                                                        LENGTH: 1920
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
NAME/KEY: CDS
LOCATION: (1)...(1917)
                                              EATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1021 GCCGGACGAGTGGCCCAGATCCGCCAGGAGATCGAGAACAGCGACTCCGACTACGACCGT 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.6%; Score 458.6; DB 9; Best Local Similarity 55.8%; Pred. No. 2.2e-102; Matches 875; Conservative 0; Mismatches 694;
961 GTCGTGGTCACCAAGGACGAGACCACCATCGTCGAGGGCGCCGGTGACACCGACGCCATC 1020
                                   975 ATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATT 1034
                                                                                                                                                                                     855 GATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACA 914
                                                                                                                                                                                                                                           781 GTCGTCAACAAGATCCGCGGCACCTTCAAGTCGGTGGCGGTCAAGGCTCCCGGCTTCGGC 840
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                                                                             901 GAAGAGGTCGGCCTGACGCTGGAGAACGCCCGACCTGTCGCTAGGCAAGGCCCGCAAG
                                                                                                                                                             841 GACCGCCGCAAGGCGATGCTGCAGGATATGGCCATTCTCACCGGTGGTCAGGTGATCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 ACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAG
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                                                                                                                     GAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAG
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                                                                                                                                                  APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PILING DATE: 2000-04-77
PRIOR FILING DATE: 2000-04-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                          SOFTWARE: PatentIn
SEQ ID NO 1
                                                                                                PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
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ORGANISM: Corynebacterium glutamicum
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                                        ENGTH: 3309400
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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Best Local Similarity
Matches 905; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         2890363 GAGCTTGAGGATCCTTACGAGAAGATCGGCGCAGAGCTGGTCAAGAAGTCGCTAAGAAG 2890304
                                                                                                                                                                                                                             312 CATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 GAATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 GAAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATC 191
432 AAGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAAGTTGGAGAGTAT 491
                                                                                                                         372 GAAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGC 431
                                                                                                                                                                                                                                                                                                                                                                            252 ACCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 CATATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTT 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.6%; Score 458.4; DB 9; Length 3 56.4%; Pred. No. 1.2e-100; tive 0; Mismatches 681; Indels
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В 20 Db 2889943 AAGGGCTACATCTCCGGTTACTTCGCAACTGACATGGAGCGCCTCGAGGCTGTTCTGGAA 2889884 Db 2890003 GTTGAAGAGTCCAACACTTTCGGTGTTGAGCTCGAGGTTACTGAGGGTATGCGCTTTGAT 288994 657 AACCCATTTATCTTAATCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTA 716 597 CGTGGTTACCTGTCTCAATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAA 656 537 ATCGAAGAATCTCGAGGTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGAC 596

2890063 ATTGCTAAGGCAATGTACGCAGTTGGCGGTGGCAAGCTGAACAAGGATTCCGTCATCACT 2890004

492 ATCTCAGAAGCTATGGAGCGTGTGGG------CAACGATGGTGTGATTACC 536

2889883 GATCCTTACATCCTGCTGGTTTCCGGCAAGATCTCCAACATCAAGGACCTGCTCCCACTG 2889824

밁 Ş 2889763 GAGGCTCTGTCCACCCTGGTTGTCAACAAGATCCGTGGCACCTTCAAGTCTGTTGCTGTT 2889704 837 AAAGCGCCAGGATTTGGTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACA-896 777 GAAGCACTTCCAACCCTTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTC 836

В 2889703 AAGGCTCCGGGCTTCGGCGACCGTCGTAAGGCTCAGCTGCAGGACATTGCTGTTCTGACC 2889644 897 GGTGGTACAGTGATTACAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCC 956 GGTGGCCAGGTCATTTCTGAAGAGGTTGGCCTCTCCCTTGAGACCGCTGATCTGCCACTT 2889584

₽ 2889583 CTAGGCCAGGCACGCAAGGTTGTTGTCACCAAGGATGACACCACCATCGTTGACGGCGCA 288952 957 CTTGGACAGGCTGCTAAGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCA 1016

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Sequence 7, Application US/10068059

Patent No. US20020155434A1

GENERAL INFORMATION:

APPLICANT: Mizzen, Lee A.

APPLICANT: Mizzen, Lee A.

APPLICANT: Siegel, Marvin

TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT

FILE REFERENCE: 12071-017002

CURRENT APPLICATION NUMBER: US/10/068,059

CURRENT FILING DATE: 2002-06-04

PRIOR APPLICATION UNMER: US 60/266,733

PRIOR FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7
                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-7
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US-10-068-059-7
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                                                               Ouery Match 27.5%;
Best Local Similarity 55.7%;
Matches 876; Conservative
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                                                                                                                                                                                                                                                                                                      LENGTH: 2130
TYPE: DNA
ONGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1554 ACAGAAGCAGTTGTTGCTAATAAACCTGAACCAGCTACGCCAGC 1597
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TTCATATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAG 69
                                                        Score 457.2; DB 9; Length Pred. No. 5e-102; 0; Mismatches 698; Indels
                                                                                                                          Length 2130;
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                                                                                                                    1030 CTATTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTG 1089
                                                                                                                                                                     1463 GCAAGGTCGTGGTCACCAAGGACGAGACCACCATCGTCGAGGGGCGCCGGTGACACCGACG 1522
                                                                                                                                                                                                                                                              1403 TCAGCGAAGAGGTCGGCCTGACGCTGGAGAACGCCGACCTGTCGCTAGGCAAGGCCC 1462
                                                                                                                                                                                                                                                                                                                                                          1343 TCGGCGACCGCCAAGGCGATGCTGCAGGATATGGCCATTCTCACCGGTGGTCAGGTGA 1402
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                                                                                                                                                                                                                                                                                                    910 TTACAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 TTGAAACAGCAACAGCAACAGCTGTTGAAAGCCTTGAAAGCCATTGCTCAACCTGTATCTG
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APPLICANT: ANDO, SELICO
APPLICANT: HAXASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OLAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1990-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 2986
LENGTH: 1644
TYPET: NAME
            S
                                                                                                                                              ; LENGTH: 1644
; TYPE; DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2986, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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       15 ATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTGAT 74
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                                                     tch 27.5%; al Similarity 56.4%; 903; Conservative
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                                                   Score 457; DB 9; 1
Pred. No. 4.9e-102;
0; Mismatches 680;
                                                                                              Length 1644;
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1080 TCTGACTTTGACCGTGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCT 1139
                                                                  1021 TCTGAGGCTCAGATCGAAGGCCGCGTCAACCAGATCCGCGTTGAGATCGAGAACTCCGAT 1080
                                                                                                             1020 AGTTCAGAAGCTATTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACA 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 GAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 AATGATATTGCTGGTGATGGGACGACTACTGCAAACAGTTTTTGACACAAGCCATTGTTCAT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CTTGAGGATCCTTACGAGAAGATCGGCGCAGAGCTGGTCAAGGAAGTCGCTAAGAAGACT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 AAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GATGACGTCGCGGGCGATGGCACCACCGCTACCGTATTGGCACAGGCTCTGGTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 TTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AAGGCTTGGGGTGCCCCAACCATTACCAACGATGGTGTCACCATCGCACGTGAGATCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ACCCTGGCTGACGCTGTTAAGGTTACTTTGGGACCAAAGGGCCCGTAACGTCGTTTTGGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 ATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACAGGCTGCTAAGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGA 1019
                                                                                                                                                                                                                                          GGCCAGGTCATTTCTGAAGAGGTTGGCCTCTCCCTTGAGACCGCTGATCTGCCACTTCTA 960
                                                                                                                                                                                                                                                                                                                                    GCTCCGGGCTTCGGCGACCGTCGTAAGGCTCAGCTGCAGGACATTGCTGTTCTGACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGAAGTTCTTAAAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGGCCTGCGCAACGTTGCTGCTGGCTCTAACCCAATGGGCATCAAGCGTGGCATCGAG
                                                                                                                                                      GGCCAGGCACGCAAGGTTGTTGTCACCAAGGATGACACCACCATCGTTGACGGCGCAGGT 1020
                                                                                                                                                                                                                                                                                      GGTACAGTGATTACAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTT 959
                                                                                                                                                                                                                                                                                                                                                                                 GCGCCAGGATTTGGTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGT 899
                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCTGTCCACCCTGGTTGTCAACAAGATCCGTGGCACCTTCAAGTCTGTTGCTGTTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTACCTGTCTCAATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAAC 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACTTCCAACCCTTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAA 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCAGATCGCTGCTACCGCTGGTATCTCCGCAGCTGACCCAGCTATCGGCGCACAGATT 480
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1561 GAGGCTGTCGTTGCTGACAAGCCACAGCCTGCAGGCGCAGC 1601
                           1557 GAAGCAGTTGTTGCTAATAAACCTGAACCAGCTACGCCAGC 1597
                                                                              1501 AAGGTCACCCGCTCCGCACTCCAGAACGCTGCATCCATTGCAGCTCTGTTCCTGACCACT 1560
                                                                                                                                                        1441 CTCAACGCTGCAAACGGCGAGTACGTCGACCTCATGGCTGCGGGCATCAACGACCCAGTT 1500
                                                                                                                                                                                                                                      1381 GCTGGCCTCGAGCCAGGCGTTGTTGCTGACAAGGTTTCCCAGCTCCCACAGGGCGAGGGC 1440
                                                                                                                                                                                                                                                                                                                1317 ACTGGACGTAACATTGTGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAAT 1376
                                                                                                                                                                                                                                                                                                                                                                                               1437 TTTAATGCTGCAACAGGTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTC 1496
                                                                                                                                                                                                                                                              1377 GCTGGGTACGAAGGCTCCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGA 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1141 GTGCTTAAGGTGGCGCAGCTACCGAGGTTGAGCTCAAGGAGCGCAAGCACCGCATTGAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1140 GTTATCAAAGTAGGAGGTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAG 1199
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